

FIGURE 1

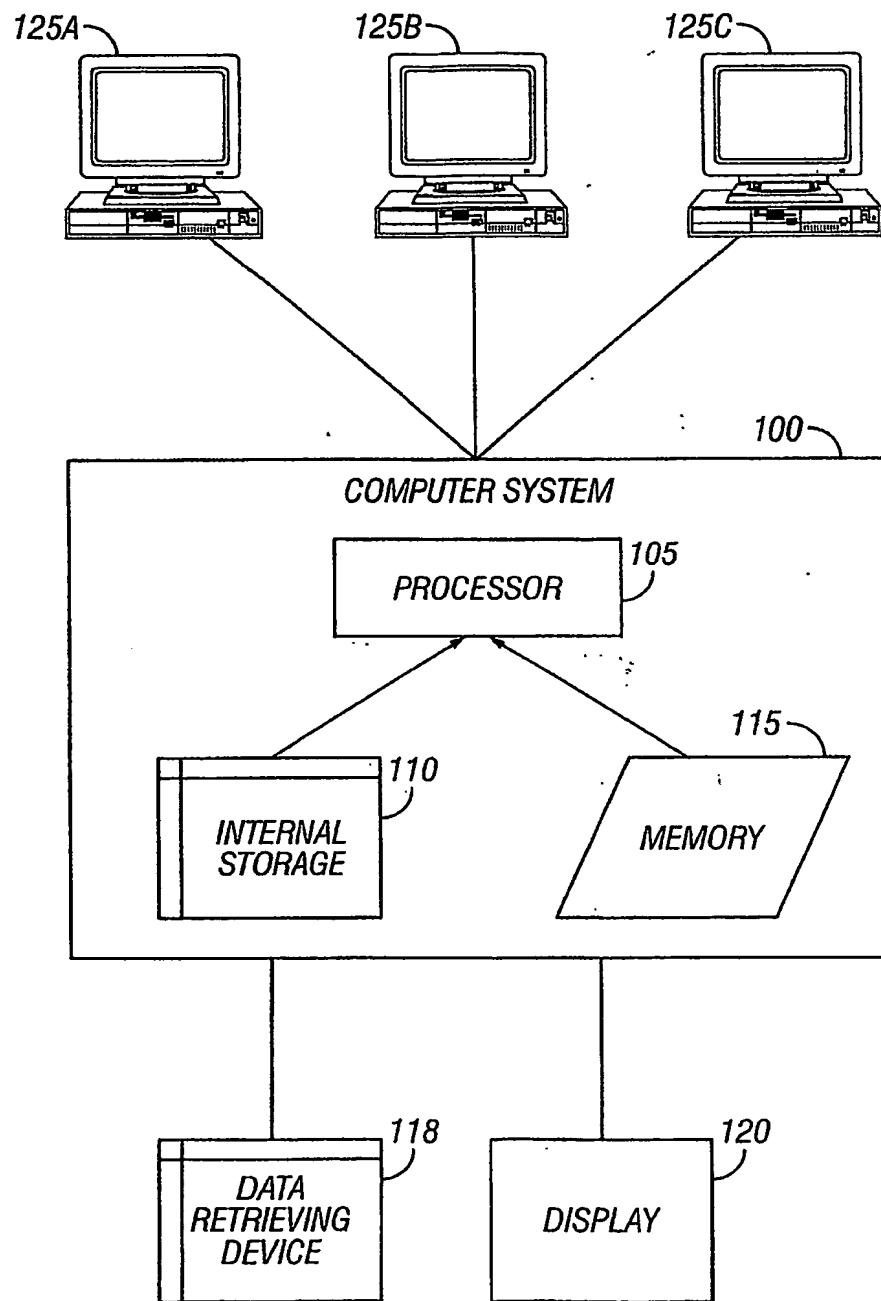


FIGURE 2

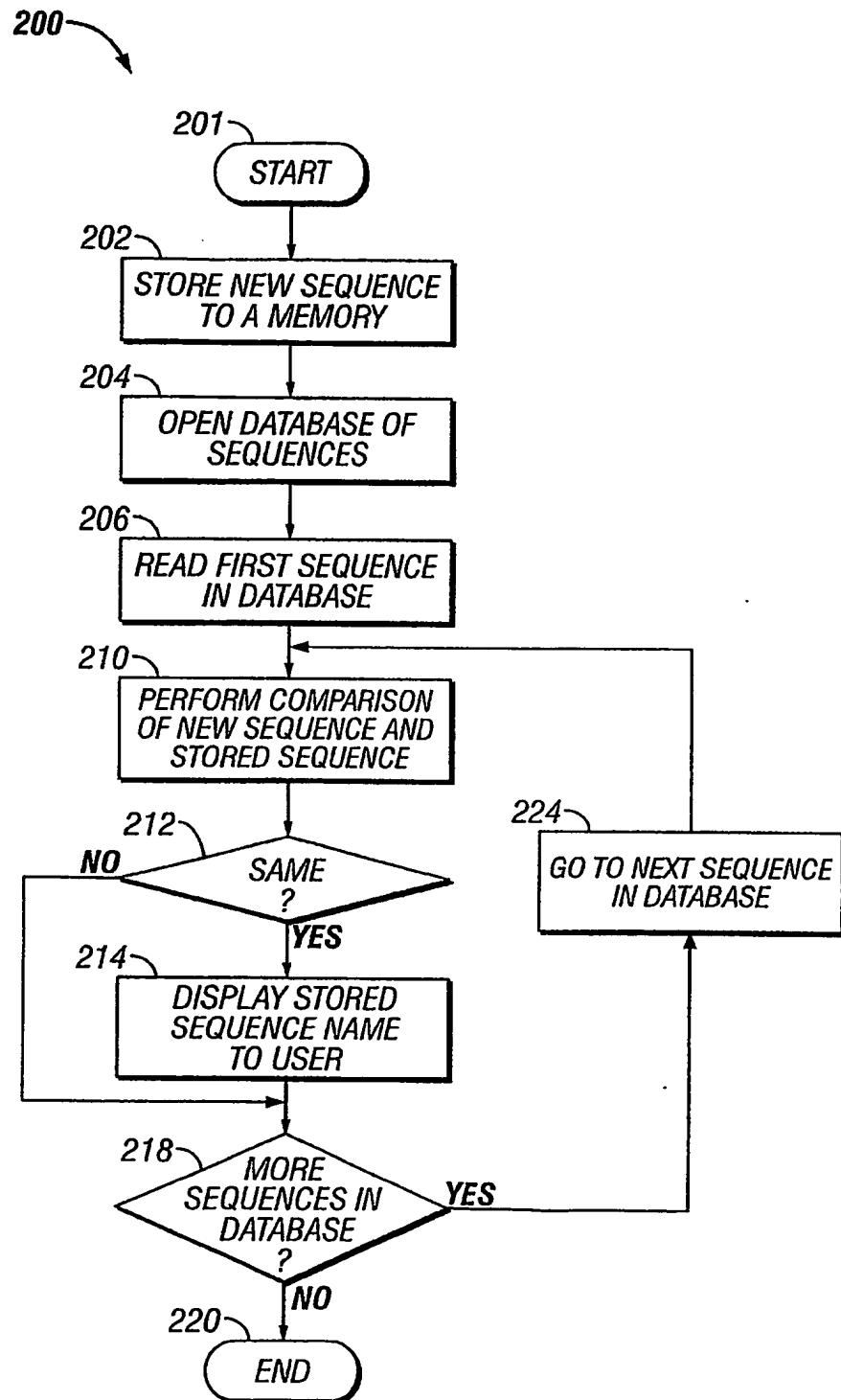


FIGURE 3

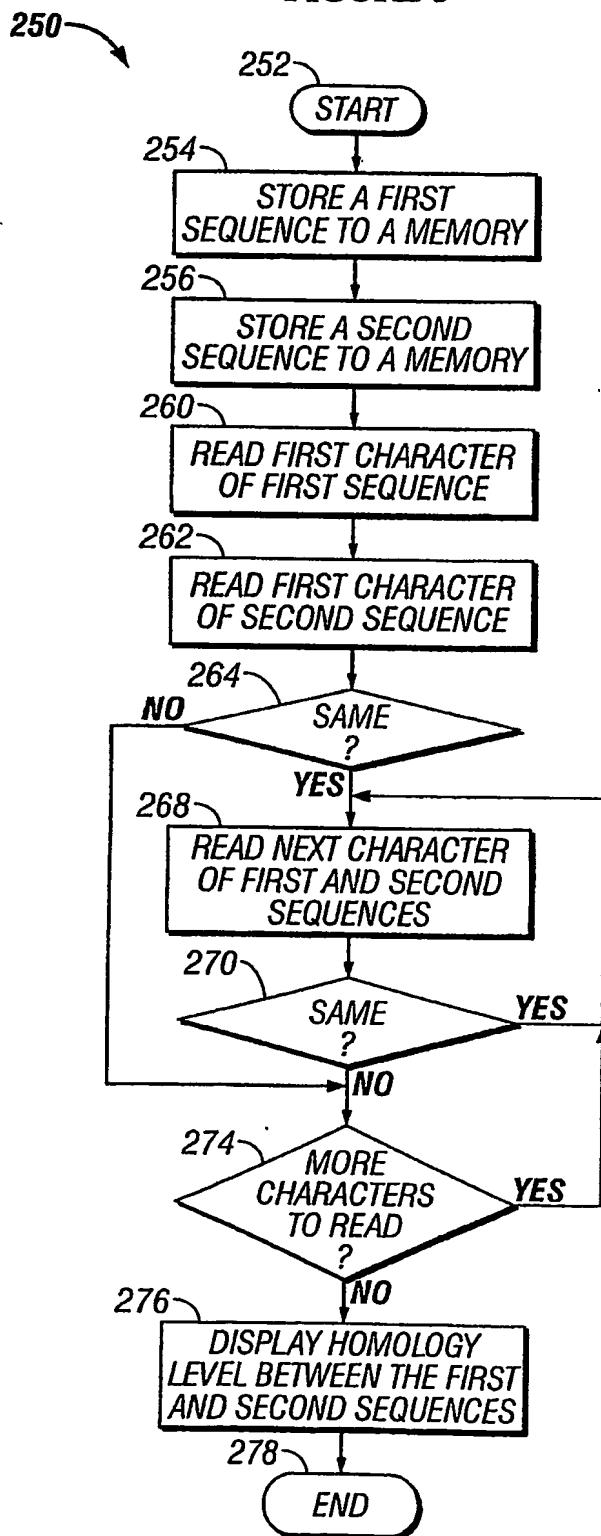


FIGURE 4

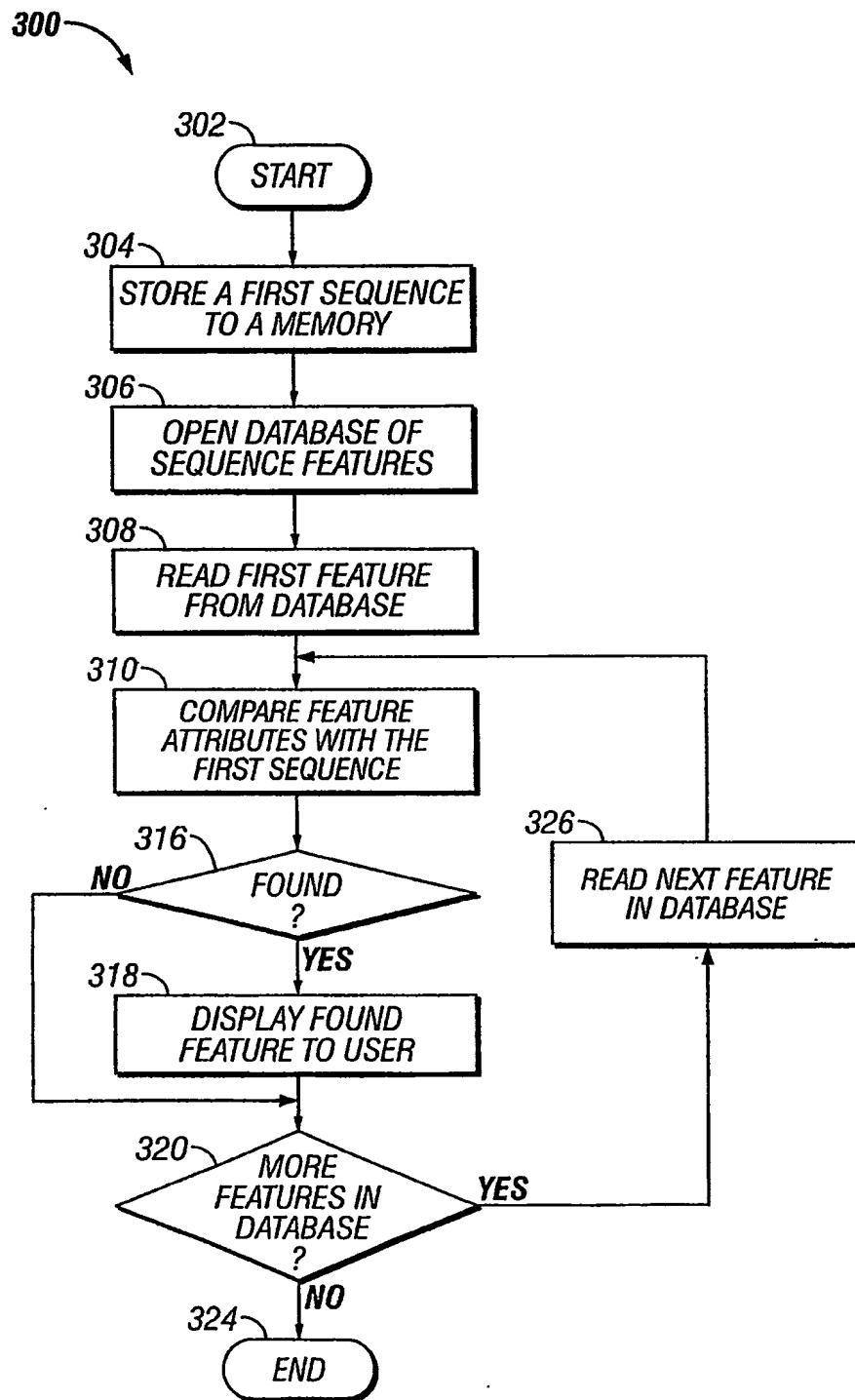


FIGURE 5

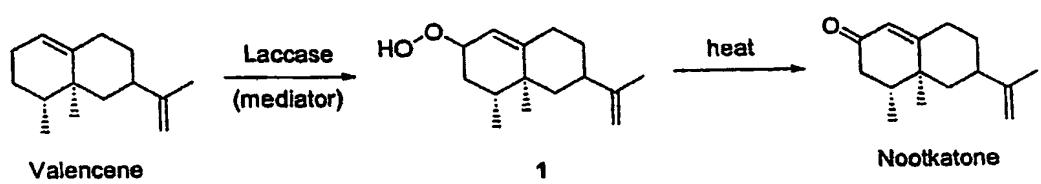


FIGURE 6

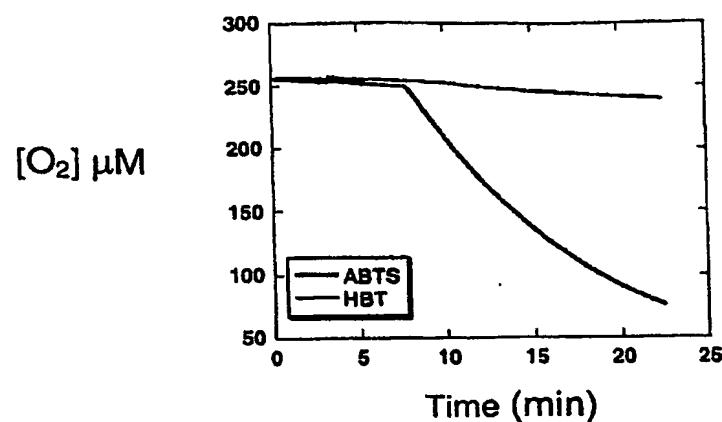


FIGURE 7

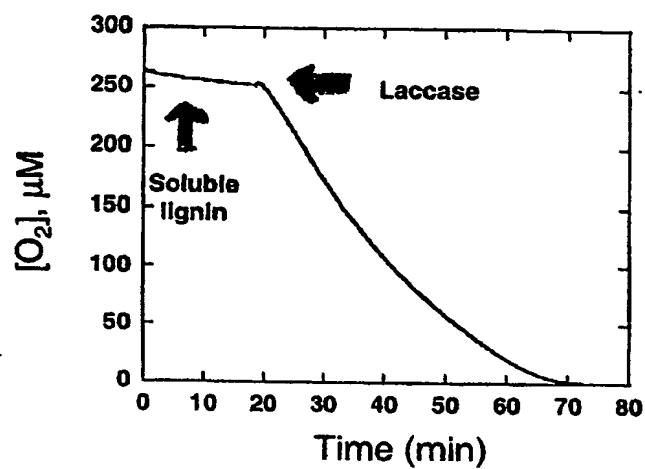


FIGURE 8

Enzyme, 57 mU	ABTS			HBT			TEMPO			Lignin, pH 9 (4 mg/ml)	
	pH 5	pH 5	pH 7	pH 5	pH 7	pH 9	pH 9	pH 9	pH 9	pH 9	pH 9
<i>T. versicolor</i>	16.5	0.52	0.08	0 ²	0 ²	0 ²	0 ²	3.0 ²	-	-	7.45 ²
<i>P. ostreatus</i>	19	-	-	-	-	-	-	-	-	-	-
SEQ ID NOS:15, 16 (expressed in <i>Pichia</i>)	17.4	0.15	0	0	0	0	0.8 ²	12.6 ²	6.2 ± 2.4	20 ± 0.35	20 ± 0.35
SEQ ID NOS:15, 16 ¹	15	TBD	0.32	0.57	-	-	-	-	-	-	-
SEQ ID NOS:9, 10 ¹	14.2	TBD	TBD	TBD	TBD	TBD	-	-	-	-	-
SEQ ID NOS:5, 6 ¹	3.6	0.37	0.1	0.1	0.1	0.1	0.31 ²	0	0	0	0
SEQ ID NOS:13, 14 ¹ (expressed in <i>Pichia</i>)	8 ³	0	0.06	0	TBD	TBD	-	-	-	-	-
SEQ ID NOS:13, 14 ¹	10.8 ³	0.16 ³	0.29	0.3	1.4 ²	1.4 ²	-	-	-	-	-
SEQ ID NOS:19, 20	5.7	0	-	-	-	-	0.08	-	-	-	-

¹includes 100 µM CuSO₄; 20.3 U enzyme; 3 pH 6

FIGURE 9

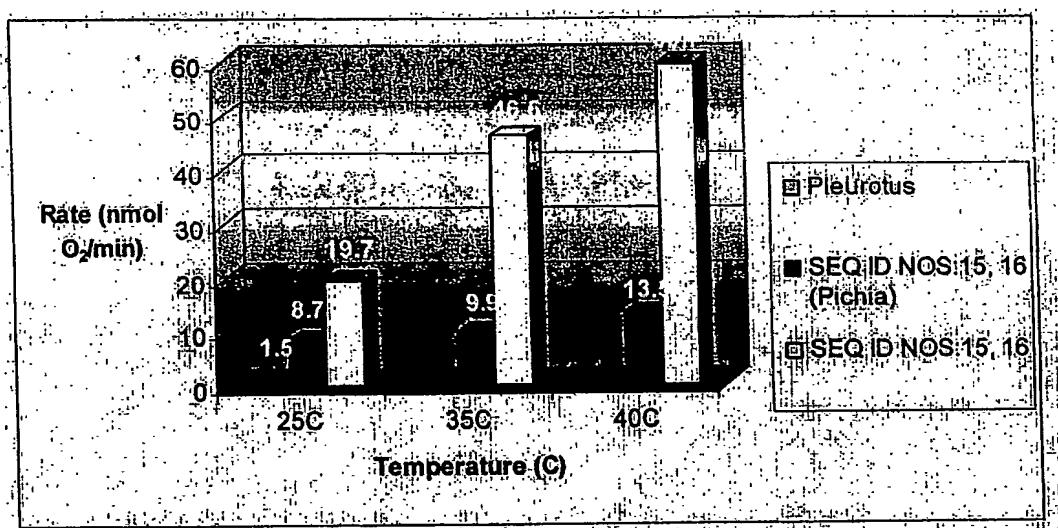


FIGURE 10

SEQ ID NO: 4	MLRPEDATRR AFLHAATMSCL VAAAGASGLLT REVRAQFRAANPQFIPDLEIQLN PREDH	60
SEQ ID NO: 8	-MDGFVESRREFI RTTG M-----AGAMLFS S QNL PAAA AADYT-----VR IKA-----AP	48
Consensus	:	27
10 20 30 40 50 60		
70 80 90 100 110 120		
SEQ ID NO: 4	V S I L P G P L T R V W R Y D G K V V K G D P G N L A F L S N G Y L P V V R V R F G Q K V R I D E V N Q L A E P T I H	120
SEQ ID NO: 8	I E I A S D K I L S T I T Y N G Q F P G -----P L T I R K E G R Q V T V D I F N E T D T P E Q I H	94
Consensus	:. * .. : . * : * ..	52
130 140 150 160 170 180		
SEQ ID NO: 4	W H G L Y V P A A M D G H P R N -----A V S T E E H Y V Y E F E I A N Q A G T W H A H E D G R T G A Q I Y F S I A	176
SEQ ID NO: 8	W H G Q F V S P D V D G A A E E G T P Y I P A H C O R R I M F T P G P A G L R F M T H N R A G A D L S L G O Y S G O V	154
Consensus	*** : * .. : * * .. : * : * ..	71
190 200 210 220 230 240		
SEQ ID NO: 4	G V L I V D D E E A A A G L E E G P Y D V P L V I Q D R I F D D R N Q F T Y L A E G N E C M G M M G N G G M M G R G	236
SEQ ID NO: 8	G P V Y I E P K E N P C R Y D E V F V L K E F E P -T I S R G G D M P Q D F L S P S A I D K T L K E T G E A A M K A	213
Consensus	* : : : : * .. : . * : * .. : * : ..	89
250 260 270 280 290 300		
SEQ ID NO: 4	G M M G G G G M Q M M P R M M G F I G D R I L V N G K P D F V L P V A A R A Y R L R I L L I N G S N P R I Y K L A W S D R	296
SEQ ID NO: 8	S L A K R M P H G Y E V G Y K F F T I N G R M L G H G E P -I R V K H G E R V L F H I L N G S A T E I R S L A L P D H	271
Consensus	.. : * .. : .. * : * : * .. : ..	115
310 320 330 340 350 360		
SEQ ID NO: 4	T P L T V I G T D G G L L E R P V T R Q V T I L A P A E R V D V W V D F S R W V G T K L T L Q S -L A F D G V I A M G	355
SEQ ID NO: 8	S -F B V I A L D G N P V P V N P V H V P V L W L G T A E R I S A V V E M M H P G V W I L G D L I A D D D R N H C M G V V	330
Consensus	: : * .. * .. : * .. : * .. * : * .. : ..	139
370 380 390 400 410 420		
SEQ ID NO: 4	G M I G N T S L E S C G A S F P V L K V E V D Q R A N T K M E L P A R L A S L P P V R F Q D A V N A H N P K V F N I T M G	415
SEQ ID NO: 8	E Y A G R S C K P H W A T P P F R W D Y A R F A K E N A S A P -----E A D E A F D M T F A K D N A A E A G	381
Consensus	* .. : * .. : * : .. : * : .. : * .. : ..	158
430 440 450 460 470 480		
SEQ ID NO: 4	M M V R G V N G R R F E M N G V A K T E T V R R N S T E I W E F R N E E S M M I M A H S M P V H G L O F R V L E R T V Q	475
SEQ ID NO: 8	F N R M T I N G V A Y P M S N E M A P A S F H I L R O G K R Y E I L R M R N -A S D D I H I H I L R H S F E L A N -----	436
Consensus	: : * .. : * .. : .. : .. : .. : ..	180
490 500 510 520 530 540		
SEQ ID NO: 4	P D F R A G Y R T L A A G I L V D D G W K D T V L L M P G E R I R L L L R F A S Y T G L F L Y H C H M L E H E D S G I M R	535
SEQ ID NO: 8	-----D A G I T K T A G V M K D V V M L G E Y Q Q L E I D E V A D N P G L T L F H C H Q Q L H M D F G F M A	486
Consensus	** * .. : .. : .. : ..	203
.....		
SEQ ID NO: 4	N Y L I Q T 541	
SEQ ID NO: 8	L F D Y V - 491	
Consensus	:	204

FIGURE 11A

FIGURE 11B

SEQ ID NO:20	-----HFPFHDLDN-----	LMLFR-----	TVNGQVNPTIYLRLPGEVQRWRFIHAGVEHYL	263		
SEQ ID NO:26	-----LVPYNNQSN-----	ATRQR-----	EVNGOLNPTIAIRPGETQRWRIANVSSDNFF	172		
SEQ ID NO:14	-----FDTRPQ-----		ILVNGKPKQPYFQVAA-RKYRLRIILNGSNQRPF	262		
SEQ ID NO:6	-----PMGHMG-----		FWGDTILVNLTPNPYMDVER-KIYRFRIILNGSNARPY	261		
Consensus			** * : . * * : .	28		
	370	380	390	400	410	420
SEQ ID NO:2	NLSDLN-G--GEFIQIGSDGGLLPRSVKLNSFSIAPAERFDILIDFAAFE-GOSIILANS	319			
SEQ ID NO:16	NLSDLN-G--GEFIQIGSDGGLLPRSVMLNSFSIAPAERFDILIDFAAFE-GOSIILANS	319				
SEQ ID NO:18	ILKFSNPN--LSEWQICNDGGFLPAPVQLSQLMSPAERADIVVDFSQFTPGEIILENT	380				
SEQ ID NO:20	PLELDG---HSLHQIAQDGIAFRSPEETDSVFLTEGNRADVLVRGG-QP-GTYYLRKQA	317				
SEQ ID NO:26	LLALAG---HTLHQIAADGNPYDEVVPRDOILLPPSERVEVLVQASTQL-GSYEFRTLL	227				
SEQ ID NO:14	EFRLSD-G--GEFTQIASDRGLLPAPYTTTLPSPAERADIVVDFSRYPGSSVVLENA	319				
SEQ ID NO:6	RLALLRGNQRMREWVILGEVGLLDTPKEVNEILVAPGERIDILVFRDASVNDVIKLYNF	321				
Consensus	: : : * : . : . : . : . : .					41
	430	440	450	460	470	480
SEQ ID NO:2	EGCGG-----DVNPETDANIMQFRVTK-PLAQKDESRK	351			
SEQ ID NO:16	EGCGG-----DVNPETDANIMQFRVTK-PLAQKDESRK	351				
SEQ ID NO:18	GP-----DEPFGGGEPDSDFDASKADTTROVMOFRVV--PLTTADTSTP	422				
SEQ ID NO:20	YDQ-----GRGEVPEDIIATVVVTGPPSFMRMLPWL	348				
SEQ ID NO:26	WGD-----DFQAEPDVVLATMVVAG--EAITPAPL	255				
SEQ ID NO:14	-----YFPEPSNKEILRFDVVR--SAYDPSSV	344				
SEQ ID NO:6	PHNLIGMGMIGMRMGMGMERGMGMGNMGNMNDGMADNSEFEVMEFRVTK--DSAYDKSIP	379				
Consensus						43
	490	500	510	520	530	540
SEQ ID NO:2	PKYLASYPSVRHERIQNLRTLKLAG--TQDQYG---RPVLL--LNN-----KRWHPVT	398			
SEQ ID NO:16	PKYLASYPSVQHERIQNLRTLKLAG--TQDQYG---RPVLL--LNN-----KRWHPVT	398				
SEQ ID NO:18	PNLLELPAITGLGAATNTQVSLNEEDSAVLFGVGPRALLGTLSEGEPEIRGWDDAIT	482				
SEQ ID NO:20	PTPAL-HRTITDEVTGSRISIVFSV--QAPAG---EMFPRFLIDG--HTFSPDRVD	397				
SEQ ID NO:26	PTALIPIYEDLRDVPVDNIRVTFFEE--PGAP-----L--YLAIDG--KHFDPDRVD	300				
SEQ ID NO:14	PARLATLPPTAAPQTQRTYTLDFDVQTGAGS-----IS-----G-----KTWDEQRVD	387				
SEQ ID NO:6	QRLSEVTPINTDGAQVQRTILGMRRMVFTIN-----GETWEDGYANP--QDINNPKV	430				
Consensus						45
	550	560	570	580	590	600
SEQ ID NO:2	EAPKAGSTEIWSIINPT-RGTHPIHLHLVSLRVLDRRPFDTARFEERGELAYTGPAPPPP	457			
SEQ ID NO:16	EAPKAGSTEIWSIINPT-RGTHPIHLHLVSLRVLDRRPFDTARFEERGELAYTGPAPPPP	457				
SEQ ID NO:18	ENPALGSIEVWEIHNFT-EDAHPHIHIEVAFEEVNRQPFEGS--ARG-----PE	528				
SEQ ID NO:20	HSIPLGSVEEWTVINNH-REDHPFHIIHVNAFEVTHLNGDRLP-----	438				
SEQ ID NO:26	QTVKLGATEEIVRNTS-SEWHPFHIIHVNDFOVIAVNNEAVN-----	341				
SEQ ID NO:14	TTVROGDTTEVWEIKNTHPFIPNFHIIHLVDFRILDIDGKPT-----PG	431				
SEQ ID NO:6	EEQNNGDVVIIEYVNT-GMYHPMHIGFOFOVLERSLGPLR-----	471				
Consensus	*	*	*	*	*	54
	610	620	630	640	650	660
SEQ ID NO:2	PSEKGWIKDTVQSHAGEVRLRHAVTFGP-YTG--RYVWHCHILEHEDYDMRPMDDVIDPHKS	514			
SEQ ID NO:16	PSEKGWIKDTVQSHAGEVRLRHAVTFGP-YTG--RYVWHCHILEHEDYDMRPMDDVIDPHK-	513				
SEQ ID NO:18	VWEGGFKDTVIAYPEEITRVKAHD--LPG--LYVWHCHIVEHEDNEMMRPy-FIGP--	580				
SEQ ID NO:20	--RPRWHDVINVPFGTATFRTRFED-FTG--KFLVHCHLLVHEDLCMMQTVEVT-----	488				
SEQ ID NO:26	--THGYEDSVALPPHSETTMRMKFLD-FSG--KFVYHCHILGHEDFGMMAVVEVVE--	392				
SEQ ID NO:14	--DAGLKDTVRIGPGETARILVHFDFPYSG--RYYYHCHLIDHSSCMYMANLEITR--	483				
SEQ ID NO:6	ATDLGWIKDTVIVAPMETVRIAVDMSHPYNEHQIYLLHCHILEHEDGMMVNVRNA--	527				
Consensus	* : . : . : . : . : . : . : . : . : .					66

FIGURE 12

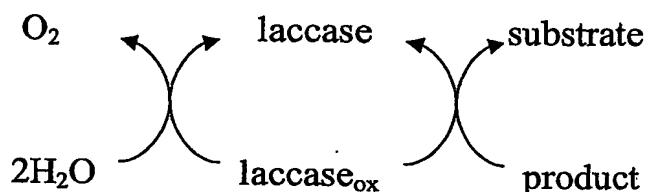


Figure 12B

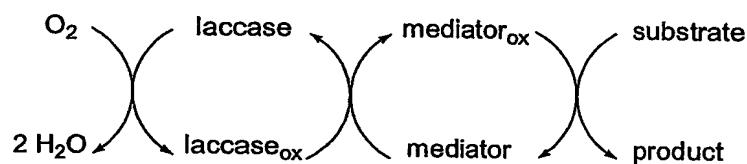


Figure 12C

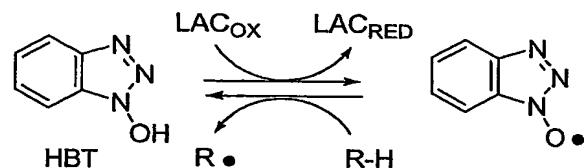


Figure 12D

